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PATENT APPLICATION



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

27/1

In re application of:

Yoji IKAWA, et al.

Appln. No.: 09/670,568

Group Art Unit: 1642

Confirmation No.: Not Yet Assigned

Examiner: N. Davis

Filed: September 27, 2000

For: HUMAN p51 GENES AND GENE PRODUCTS THEREOF

SUBMISSION OF FORMAL DRAWINGS

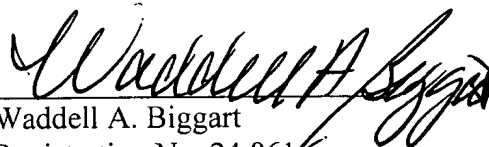
Commissioner for Patents
Washington, D.C. 20231

Sir:

Submitted herewith please find 15 sheets, (Figures 1-15) of formal drawings. The

Examiner is respectfully requested to acknowledge receipt of these formal drawings.

Respectfully submitted,


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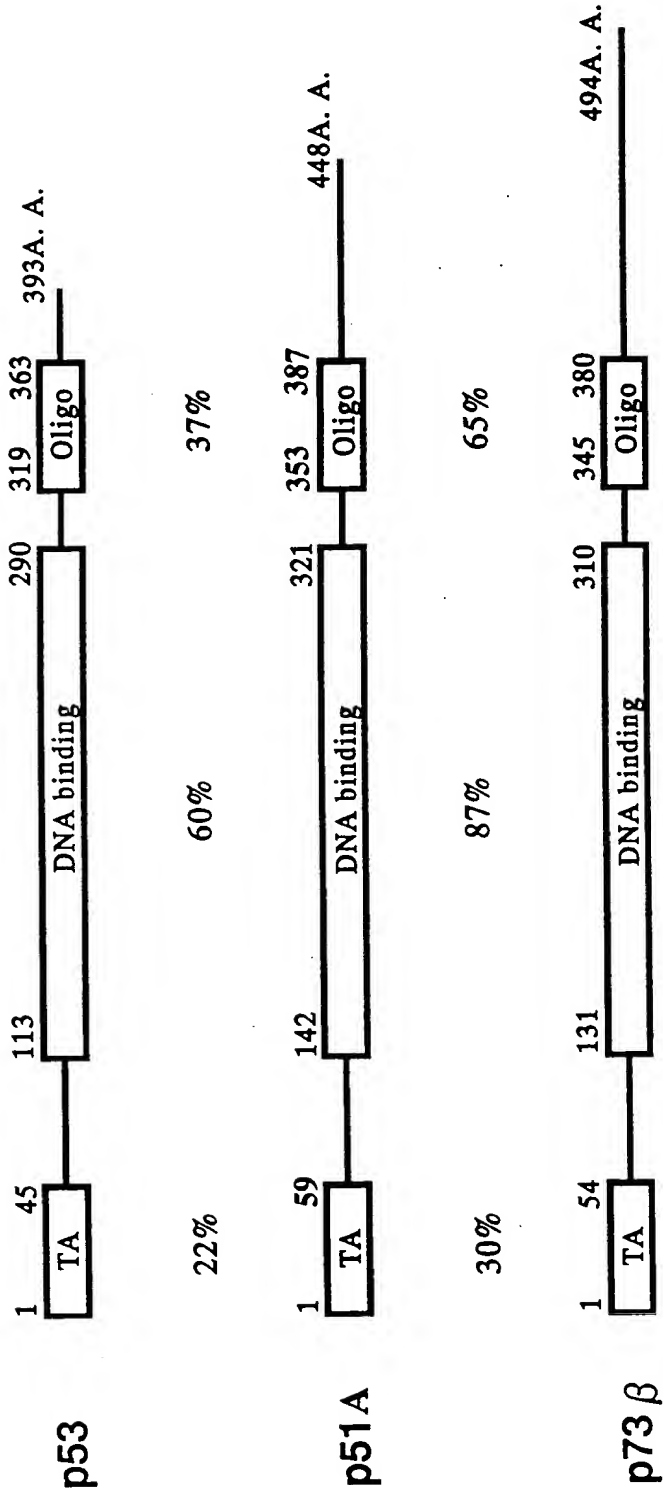
Date: May 11, 2001

APPROVED	O.G. FIG. 1
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FIG. 1



APPROVED	O.G. FIG.	
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FIG. 2

p51A	MSQSTQTNEF	LSPEVFQHIW	DLLEQPICSV	QPIQLNFVDE	PSIEDGATNKI	50
p73B	MAQSTATSP-	DGGTTFEHLW	SSLE-POSTY	--FQLP-QSS	RCNNEWVGGT	45
p53	KEEPQSDPS-	VEPPLSQETF	SQI-----	--WHL-----L	PENNVLSPLP	36
Consensus	M.QST.T...	..P..FQH.W	SLE-P....	---DL.....	P.NN.....	50
p51A	EISMDCIRMQ	DSOLSDPMMP	QYTNLGLLS	MDQQIQNGSS	STSPYNTDHA	100
p73B	DSSMDVFHLE	--GMTTSVMA	QF---NLLSS	TMDQSSRAA	SASFYTPPEHA	90
p53	SOAMDLMLS	----PODI-E	QW----FTED	PGPDEAPRMP	EAAFR-RVARA	76
Consensus	..SMD...L.	-----D....	Q.---.LL.S	...Q...R..	SASEY...HA	100
p51A	QNSVTAPSPY	ACPSSTFDAL	SPSPAIPSNL	DYHOPHSFDV	SFOQSSSTAKS	150
p73B	-ASVPTHSPY	ACPSSTFDTH	SPAPVIPSNT	DYHOPHFEV	TFOQSSSTAKS	139
p53	-PAAPTAA-	PAPAPSW-PL	SSS--VPSOK	TYQSYQFRL	QFLHSSTAKS	121
Consensus	--SVPTSPY	ACPSSTFD.L	SPSP..IPSNT	DYHOPH.E.V	EQQSSSTAKS	150
p51A	ATHTYSTELK	KLYCQIAKTC	FIQINVTTP	PDQAVIRAMP	VYKKAENHTE	200
p73B	ATHTYSPULK	KLYCQIAKTC	FIQINVSTTP	PDQTAIRAMP	VYKKAENHTE	189
p53	VHTYSPALN	KMFQIAKTC	FVQLVNSTP	PDQTRVRAMP	VYKQSOHATE	171
Consensus	ATHTYSP.LK	KLYCQIAKTC	FIQIN..TRP	PDQ..TRAMP	VYKKAENHTE	200
p51A	VVNRCPNHEL	SREFNEQQA	FPSHLIRVEG	NSHAGVVECP	VTQROSVNVR	250
p73B	VVNRCPNHEL	GRDFNEQQA	FASHLIRVEG	NNLSQVVECP	VTQROSVNVR	239
p53	VVNRCPNHEL	CSD-SQC-LA	FPCHLIRVEG	NLRVEYLQCR	NTERFSVNVR	219
Consensus	VVNRCPNHEL	.RDFNEQQA	FPSHLIRVEG	N...QVVECP	VTQROSVNVR	250
p51A	YEPFQVQTEF	TTIUYNMCHN	SSQGGQNR	PIIITITLET	RQOQLGRRC	300
p73B	YEPFQVQTEF	TTIUYNMCHN	SSQGGQNR	PIIITITLEM	RQOQLGRRS	289
p53	YEPFQVQSDC	TTIUYNMCHN	SSQGGQNR	PIIITITLED	SSQNLGRNS	269
Consensus	YEPFQVQTEF	TTIUYNMCHN	SSQGGQNR	PIIITITLE.	RQOQLGRS	300
p51A	FEFRICACPG	RDRKAEESI	RKQVSD--S	TKNGDGKRP	FRQNTGHI-Q	347
p73B	FEFRICACPG	RDRKAEEDHY	REQQALNESS	AKNGAASKRA	FKQSPPAVPA	339
p53	FEFRICACPG	RDRTEENL	RKKGEPH--H	ELPPGSTKRA	LPNMTSS---	314
Consensus	FEFRICACPG	RDRKAEED..	RKQQ....-S	.KNG..TKRA	F.QNT.....	350
p51A	H-TSINKRRS	PDDELLYLPV	RGRETYEMLL	KINLESLEIMQ	YLPQHTIETY	396
p73B	LGAGVKKRRH	QEDTYLQV	RGRNREILM	KLHESLEIME	LVPQPLVDSY	389
p53	--SPQPKKPK	LDGEYFTLQI	RGRERREMR	ELHBALEIKD	AQAGKEPGGS	362
ConsensusKRR.	LD.E...YLV	RGR..REML.	KLHESLEIM.	..PQ.....Y	400
p51A	RQOQQQQHQ-	HL-----	---LQ-H-	-LLSACFRNE	LV-EPRRE--	427
p73B	RQOQQLLRP	SHLQPPSYGP	VLSPMNVHG	GANKLPSVNO	LVGQPPPHSS	439
p53	RAHSS-----	HL-----	-----K-	-----SKKGQ	---STSRH--	380
Consensus	RQOQQ....	HL-----	---LQ-H-	-----NQ	LV-.P.RH--	450
p51A	--TPKQSDV-	--FFR---HS	KPPN-----	-----RSVYP-	-----	448
p73B	AATPNLGPVG	PCMLNNHGA	VPANGEMSSS	HSAQSMVSGS	HCTPPPPYHA	489
p53	---KKL----	---MFK---T	EGPD-----	-----SD---	-----	393
Consensus	--TPKL..V-	---MF---H.	.PPN-----	-----S.Y.-	-----	500
p51A	-----	-----	-----	-----	-----	448
p73B	DPSLVRTWGP	-----	-----	-----	-----	499
p53	-----	-----	-----	-----	-----	393
Consensus	-----	-----	-----	-----	-----	510

APPROVED	O.G. FIG.
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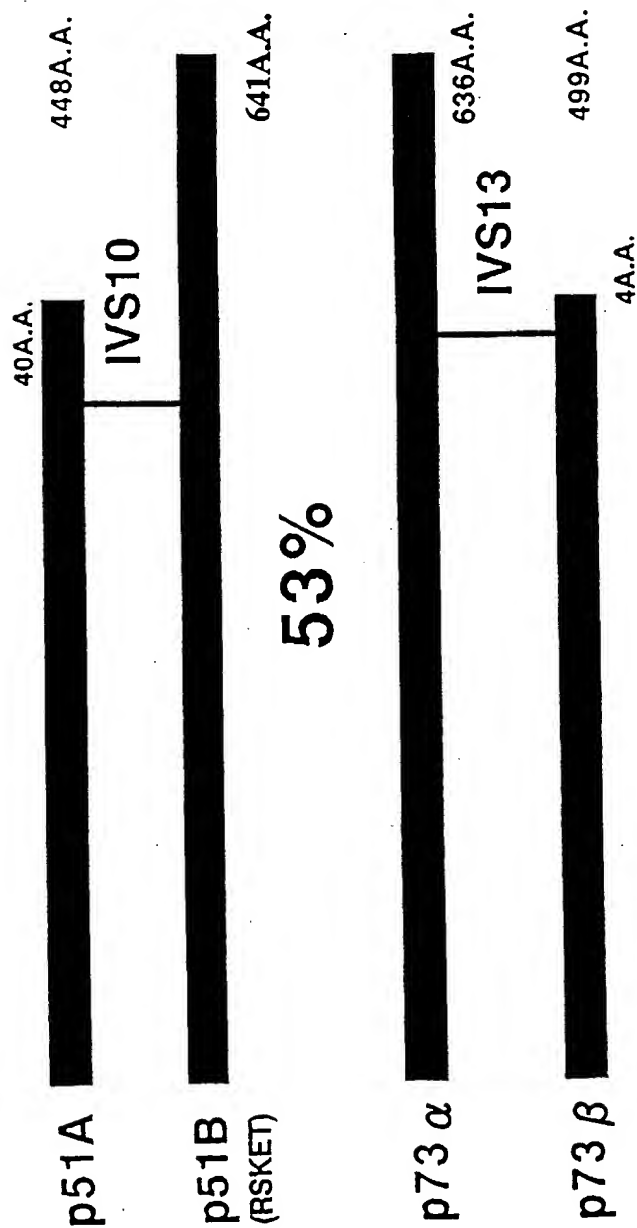
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FIG. 3

p51B	MSQSTOTNEF LSPEYFCH IN DMLLOFICSV QP DUNFVDE PSDEGATNKI	50
p73d	MAQSTATISP DGGTTHHLLW SSLE PDSTY --RDLF--QSS RGNNEVVGGT	45
Consensus	MSQST... ..LSPEY... ..IN... ..DMLLO... ..ICSV... ..QP... ..DUNFV... ..DE... ..PSDEG... ..ATNKI... ..	50
p51B	E SMCIRMQ DSDLSDFMMP QYTNLCILHS MDOQIOWGSS SISPYNTEHA	100
p73d	DSMCIVFHE --GNTTSVMA QF---MLUSS TMDQMSRAA SASPYTPBHA	90
Consensus	..SMC... ..DSDLS... ..DFMMP... ..QYTNL... ..CILHS... ..MDOQI... ..OWGSS... ..SISPYN... ..TEHA... ..	100
p51B	QMSVTAHSPY AQPSTFEAL SPSRAIPSNT DYPGPHFQV SFQQSSTAKS	150
p73d	-ASVPTHSPY AQPSTFOTM SFAFVIPSNT DYPGPHFEV TFQQSSTAKS	139
Consensus	..SV... ..SPY... ..AQPSTFE... ..SPSRA... ..IPSNT... ..DYPGPH... ..FQV... ..SFQQS... ..STAKS... ..	150
p51B	ATWTYSTELK KLYCQIAKTC PIQIKVTPP PQAVIRAMP VYKKAHVTE	200
p73d	ATWTYSPULK KLYCQIAKTC PIQIKVSTPP PQTAVIRAMP VYKKAHVTD	189
Consensus	ATWTYS... ..LK... ..KLYCQIAKTC... ..PIQIKV... ..TPP... ..PQAVIRAMP... ..VYKKAHVTE... ..	200
p51B	VVKRCPNHEL SRFNEGQIA FASHLIRVEG NSHAQYVEDP DTGRQSVLVR	250
p73d	VVKRCPNHEL SRFNEGQSA FASHLIRVEG NNLQYVEDP DTGRQSVLVR	239
Consensus	VVKRCPNHEL... ..RFNEGQ... ..IA... ..FASHLIRVEG... ..NSHAQYVEDP... ..DTGRQSVLVR... ..	250
p51B	YEPPQVGTEF TILYNFMCN SSCVGGMNR PILIINTLET RDGQVLGRRC	300
p73d	YEPPQVGTEF TILYNFMCN SSCVGGMNR PILIINTLEM RDGQVLGRFS	289
Consensus	YEPPQVGTEF... ..TILYNFMCN... ..SSCVGGMNR... ..PILIINTLET... ..RDGQVLGRRC... ..	300
p51B	FEARICACPG RDRKADEDSI RQCVSD--S TKNDGTRKP FFRONTHGI-Q	347
p73d	FEARICACPG RDRKADEDSY RQCALNESS AKNGAASKRA FRCSPPAVPA	339
Consensus	FEARICACPG... ..RDRKADE... ..SI... ..RQCVSD... ..--S... ..TKNDGTRKP... ..FFRONTHGI-Q... ..	350
p51B	M-TS KKRRS FDELLYLV RGRITYEHL MKESLELMQ YLPQHTIET	396
p73d	LGAGVKKRRS QEDTYLVV RGRNFELM MKESLELME LVPQPLVDSY	389
ConsensusKKRRS... ..FDELLYLV... ..RGRITYEHL... ..MKESLELMQ... ..YLPQHTIET... ..	400
p51B	RQQQQCHH LLKQTSICS PSYQNSSRP LNMN-SMNK LPSVQLINP	445
p73d	R----QQQ LLQRPSHLC PPSYQPLSP NMNVHGQMNK LPSVQLVQ	433
Consensus	R... ..Q... ..Q... ..LLQ... ..TSICS... ..PSYQNSSRP... ..LNMN-SMNK... ..LPSVQLINP... ..	450
p51B	QQRNALTPTT IPOGQANIP MAGTHPMAG DANGLSPTQA LPPPLSMFST	495
p73d	PPPHSSAATP NLGPVCPG-- MLNNHGHAVP ANGENSSSH-- --SACSMSG	478
ConsensusT... ..T... ..IPOGQANIP... ..MAGTHPMAG... ..DANGLSPTQA... ..LPPPLSMFST... ..	500
p51B	SHCTPPPPYP TQSSIVGFLA RLGGSSGLDY FTIQGLTIY QIEHYSMDOL	545
p73d	SHCTPPPPYH AQPSSVFLT GLGPNQIEY FTSQGLQSIY HLQNLTIEDL	528
Consensus	SHCTPPPPY... ..TQSSIVGFLA... ..RLGGSSGLDY... ..FTIQGLTIY... ..QIEHYSMDOL... ..	550
p51B	ASLKIPEQRR HAINNGLCH RQHEFSSPS HLLRTPSAS TVSVGSSTR	595
p73d	GALKIPEQRR MIMHGLQOL KQHDYSTAQ QLLRSSNAT ISIQGSQELQ	578
Consensus	..LKIPER... ..R... ..HAINNGLCH... ..RQHEFSSPS... ..HLLRTPSAS... ..TVSVGSSTR... ..	600
p51B	GRVIAVWF TURTTSFP R-----DE RNDFFQMDA RRNKQRIKE	638
p73d	RQVMEAVF RVHTTTFN RGGPGGGDE MADHGFQLPD CKARKRIKE	628
Consensus	..RV... ..AV... ..F... ..TURTTSFP... ..R-----DE... ..RNDFFQMDA... ..RRNKQRIKE... ..	650
p51B	--EQL--	641
p73d	EFTAEIH	636
Consensus	..E... ..E... ..	658

FIG. 4

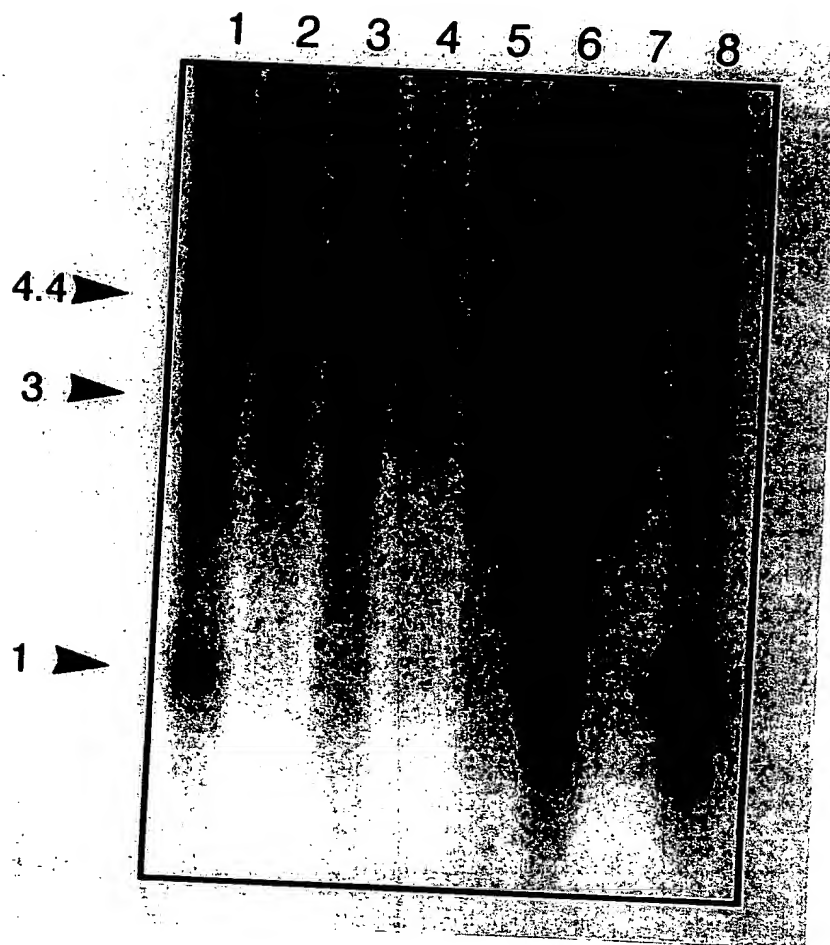


APPROVED	O.G. FIG.	
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FIG. 5

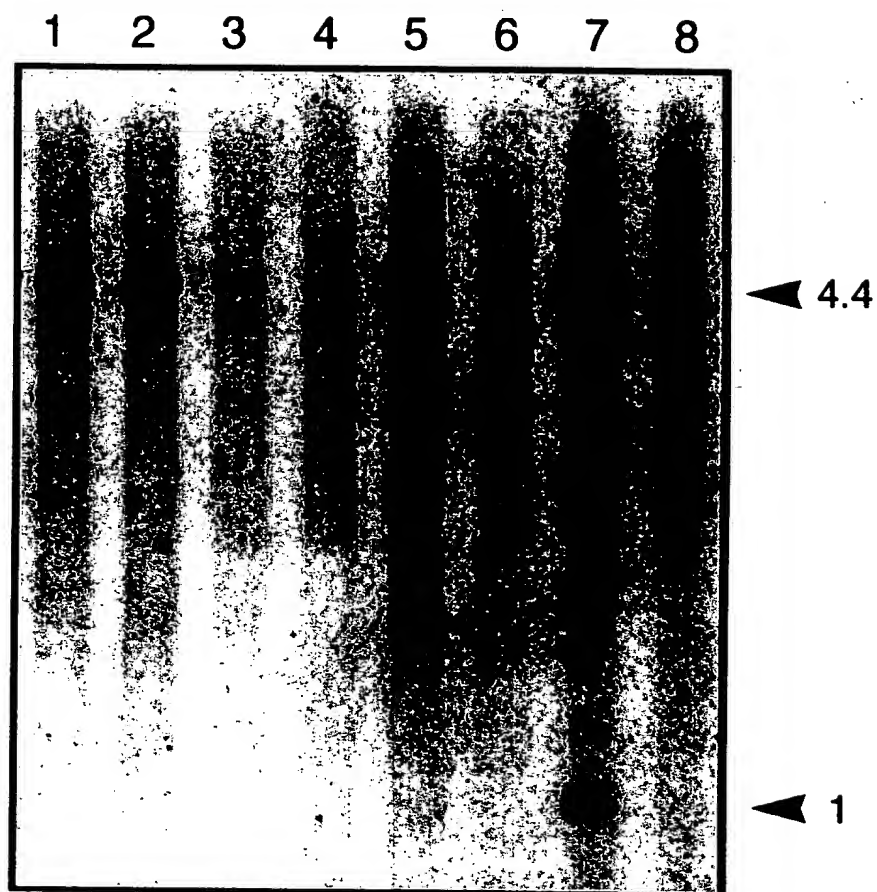


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FIG. 6

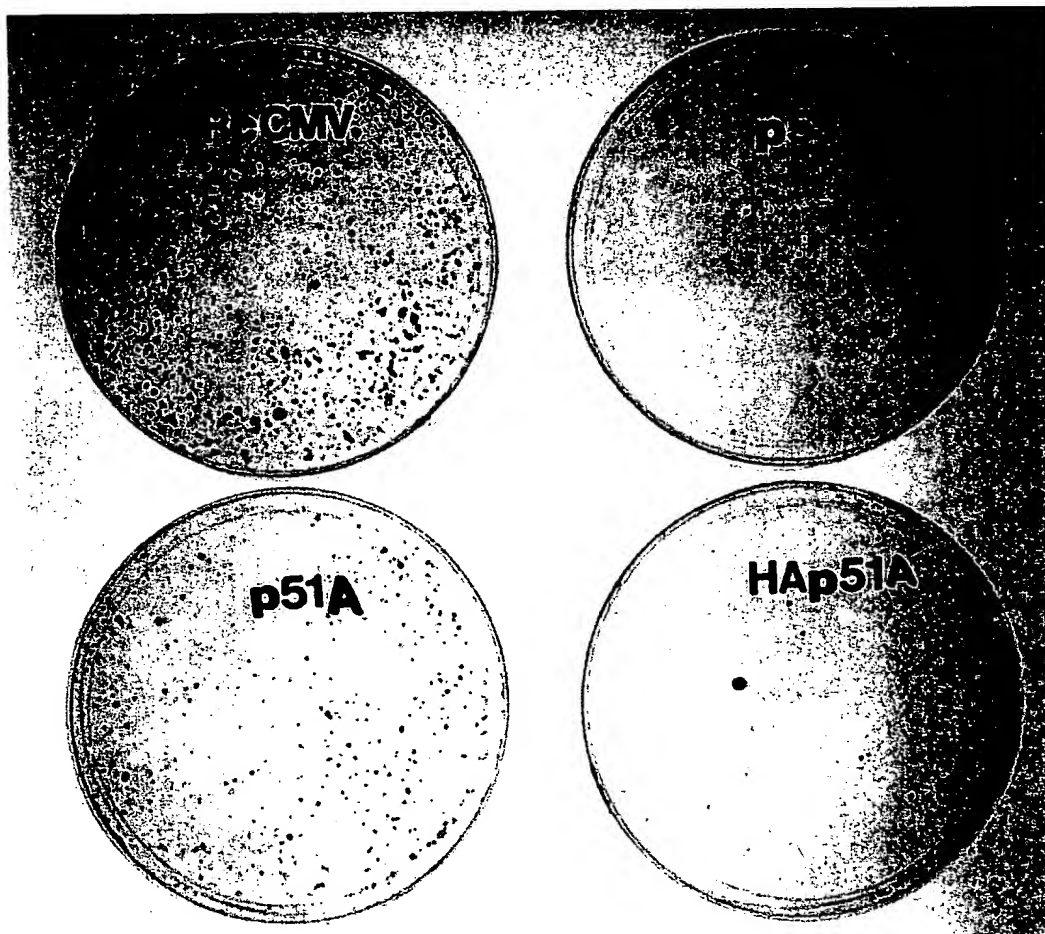


APPROVED	O.G. FIG.	
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FIG. 7

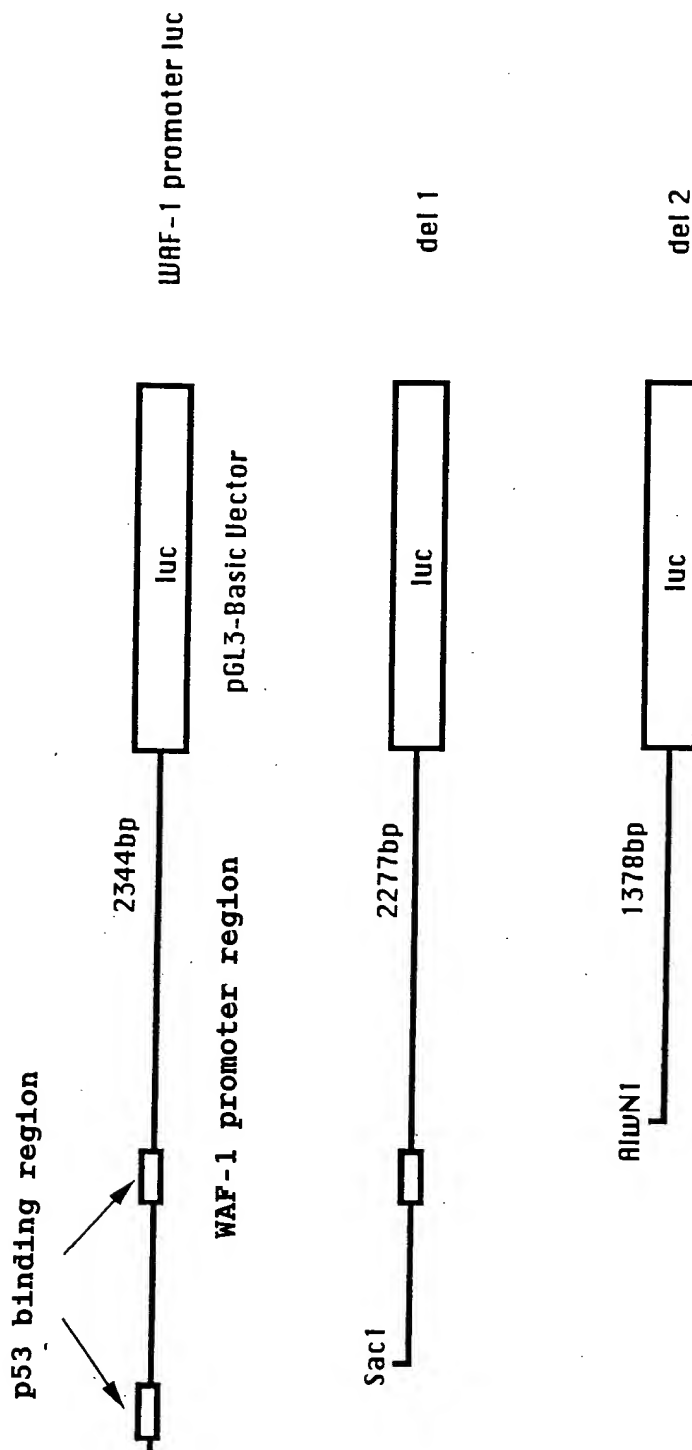


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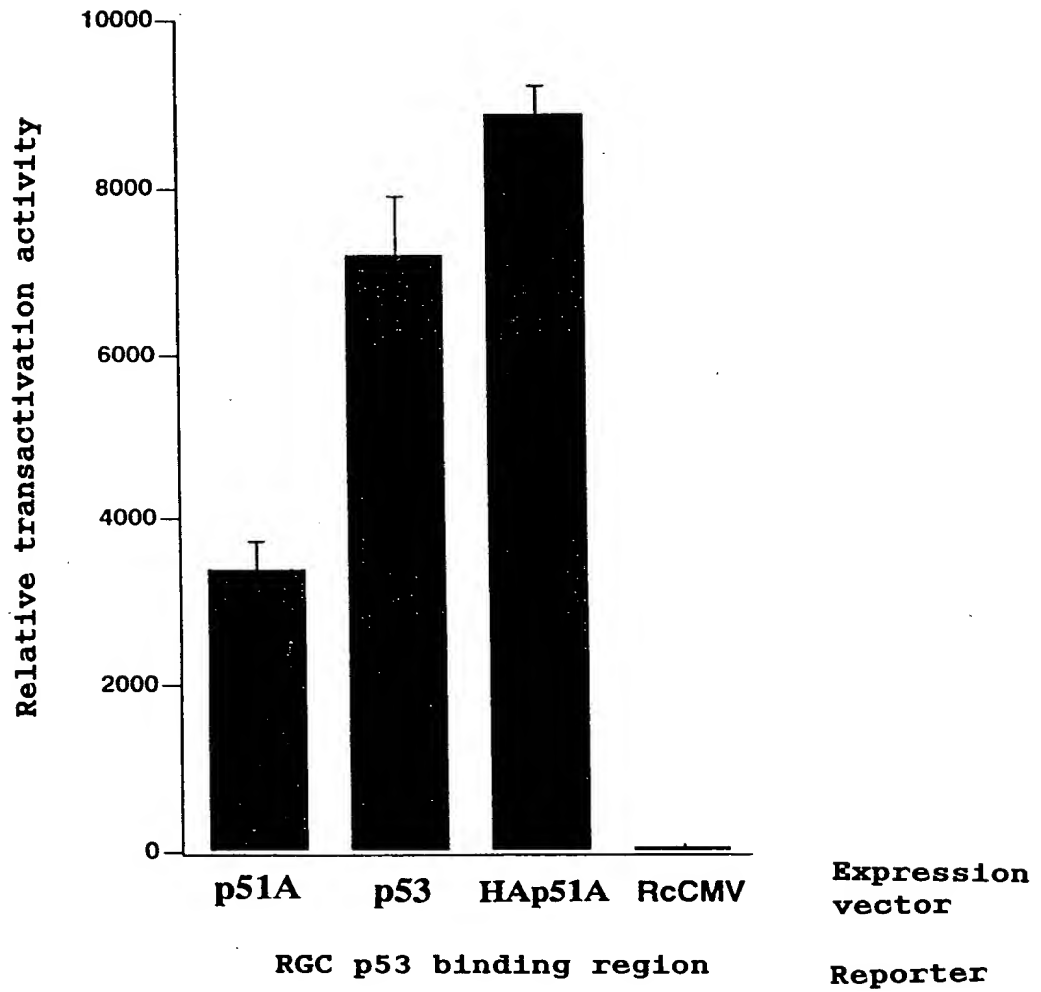
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FIG. 8



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FIG. 10

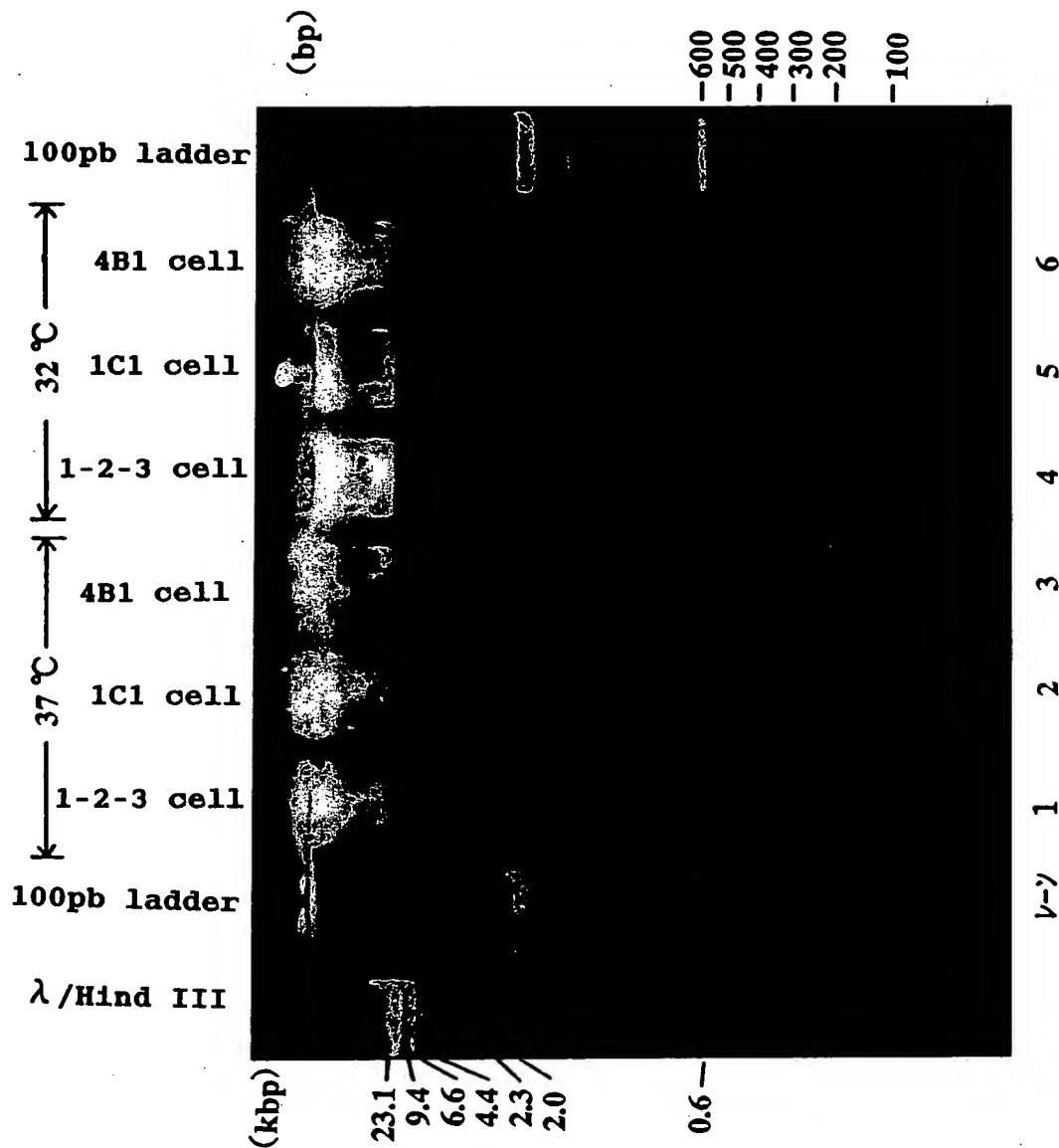


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FIG. 11



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FIG. 12

mp51	1	ATGTCGCAGAGCACCCAGACAAGCGAGTTCCTCAGCCCAGAGGTCTTCCAGCATATCTGG	60
p51B	1	ATGTCCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG	60
		***** **	
mp51	61	GATTTTCTGGAACAGCCTATATGCTCAGTACAGCCCATCGAGTTGAACTTTGTGGATGAA	120
p51B	61	GATTTTCTGGAACAGCCTATATGCTCAGTTCAGCCCATTGACTTGAACCTTTGTGGATGAA	120

mp51	121	CCTTCCGAAAATGGTGCAACAAACAAGATTGAGATTAGCATGGATTGTATCCGCATGCAA	180
p51B	121	CCATCAGAAGATGGTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCCAG	180
		** ** *	
mp51	181	GACTCAGACCTCAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC	240
p51B	181	GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC	240

mp51	241	ATGGACCAGCAGATTGAGAACGGCTCCTCGTCCACCAGCCCCTACAACACAGACCACGCA	300
p51B	241	ATGGACCAGCAGATTGAGAACGGCTCCTCGTCCACCAGTCCCTATAACACAGACCACGCG	300

mp51	301	CAGAATAGCGTGACGGCGCCCTCGCCCTATGCACAGCCCAGCTCCACCTTTGATGCCCTC	360
p51B	301	CAGAACAGCGTGACGGCGCCCTCGCCCTACGCACAGCCCAGCTCCACCTTCGATGCTCTC	360

mp51	361	TCTCCATCCCTGCCATTCCCTCCAACACAGATTACCCGGGCCCCACACAGCTTCGATGTG	420
p51B	361	TCTCCATCACC CGCCATCCCTCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG	420
		***** **	
mp51	421	TCCTTCCAGCAGTCAAGCACTGCCAAGTCAGCCACCTGGACGTATTCACCCGAACCTGAAG	480
p51B	421	TCCTTCCAGCAGTCAAGCACTGCCAAGTCAGCCACCTGGACGTATTCACCTGAACCTGAAG	480

mp51	481	AAGCTGTACTGCCAGATTGCGAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCC	540
p51B	481	AAACTCTACTGCCAATTGCAAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT	540
		** ** *	
mp51	541	CCACAGGGCGCTGTTATCCGTGCCATGCCTGTCTACAAGAAAGCTGAGCATGTCACCGAG	600
p51B	541	CCTCAGGGAGCTGTTATCCGCGCCATGCCTGTCTACAAAAAAGCTGAGCACGTCACGGAG	600
		** *****	
mp51	601	GTTGTGAAACGATGCCCTAACCATGAGCTGAGCCGTGAGTTCAATGAGGGACAGATTGCC	660
p51B	601	GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGGACAGATTGCC	660
		** *****	
mp51	661	CCTCCCAGTCATCTGATTGAGTAGAAGGGAACAGCCATGCCCAGTATGTAGAAGATCCT	720
p51B	661	CCTCCTAGTCATTTGATTGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC	720

mp51	721	ATCACGGGAAGGCAGAGCGTGCTGGTCCCTTATGAGCCACCACAGGTTGGCACTGAATTC	780
p51B	721	ATCACAGGAAGACAGAGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC	780

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FIG. 13

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mp51 781 ACBACAGTCCTGTACAATTTTCATGTGTAACAGCAGCTGCGTCGGAGGAATGAACAGACGT 840
p51B 781 ACBACAGTCCTGTACAATTTTCATGTGTAACAGCAGTTGTGTTGGAGGGATGAACCGCCGT 840
      ** ***** **

mp51 841 CCAATTTTAATCATCGTTACTCTGGAACCCAGAGATGGGCAAGTCCTGGGCCGACGGTGC 900
p51B 841 CCAATTTTAATCATGTTACTCTGGAACCCAGAGATGGGCAAGTCCTGGGCCGACGGTGC 900
      *****

mp51 901 TTTGAGGCCCGGATCTGTGCTTGCCAGGAAGAGACCCGAAGGCAGATGAAGACAGCATC 960
p51B 901 TTTGAGGCCCGGATCTGTGCTTGCCAGGAAGAGACAGGAAGGCAGATGAAGATAGCATC 960
      *****

mp51 961 AGAAAGCAGCAAGTATCGGACAGCGCAAAGAACGGCGATGGTACGAAGCGCCCTTTCCGT 1020
p51B 961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGGTACGAAGCGCCCGTTTCGT 1020
      *****

mp51 1021 CAGAATACACACGGAATCCAGATGACTTCCATCAAGAAACGGAGATCCCCAGATGATGAG 1080
p51B 1021 CAGAACACACATGGTATCCAGATGACATCCATCAAGABACGAAGATCCCCAGATGATGAA 1080
      *****

mp51 1081 CTGCTGTACCTACCAAGTGAGAGGTCGTGAGACGTACGAGATGTTGCTGAAGATCAAAGAG 1140
p51B 1081 CTGTTTACTTACCAAGTGAGGGGCCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140
      *** *

mp51 1141 TCCTGGAGCTCATGCAGTACCTCCCTCAGCACACGATCGAAACGTACAGGCAGCAGCAG 1200
p51B 1141 TCCCTGGAACTCATGCAGTACCTTCCTCAGCACACAATTGAAACGTACAGGCACAGCAA 1200
      ** *****

mp51 1201 CAGCAGCAGCACCAGCACCTACTTCAGAAACAGACCTCGATGCAGTCTCAGTCTTCATAT 1260
p51B 1201 CAGCAGCAGCACCAGCACCTACTTCAGAAACAGACCTCAATACAGTCTCCATCTTCATAT 1260
      *****

mp51 1261 GGCAACAGTTCCTCCCTCTGAACAAAATGAACAGCATGAACAAGCTGCCTTCCGTGAGC 1320
p51B 1261 GGTAACAGTTCCTCCCTCTGAACAAAATGAACAGCATGAACAAGCTGCCTTCTGTGAGC 1320
      ** *****

mp51 1321 CAGCTTATCAACCCACAGCAGCGCAATGCCCTCACTCCCACCACCATGCCGTGAGGGCATG 1380
p51B 1321 CAGCTTATCAACCCCTCAGCAGCGCAACGCCCTCACTCCTACAACCATTCCTGATGGCATG 1380
      *****

mp51 1381 GGAGCCAACATTCCCTATGATGGGCACTCACATGCCAATGGCTGGAGACATGAATGGACTC 1440
p51B 1381 GGAGCCAACATTCCCATGATGGGCACCCACATGCCAATGGCTGGAGACATGAATGGACTC 1440
      *****

mp51 1441 AGCCCTACCCAAGCTCTCCCTCCCTCACTCTCCATGCCCTCCACCTCCCACTGCACCCCA 1500
p51B 1441 AGCCCCACCCAGGCACTCCCTCCCGCACTCTCCATGCCATCCACCTCCCACTGCACCCC 1500
      *****

mp51 1501 CCACCGCCCTACCCACAGACTGCAGCATTGTGAGTTTCTTAGCAAGGTTGGGCTGCTCA 1560
p51B 1501 CCACCTCCGTATCCACAGATTGCAGCATTGTGAGTTTCTTAGCGAGGTTGGGCTGTTCA 1560
      *****
  
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APPROVED	O.G: FIG.	
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FIG. 14

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mp51 1561 TCATGCCTGGACTATTTACGACCCAGGGGCTGACCACCATCTATCAGATTGAGCATTAC 1620
p51B 1561 TCATGTCTGGACTATTTACGACCCAGGGGCTGACCACCATCTATCAGATTGAGCATTAC 1620
*****

mp51 1621 TCCATGGATGATTTGGCAAGTCTGAAGATCCCTGAACAGTTCCGACATGCCATCTGGAAG 1680
p51B 1621 TCCATGGATGATCTGGCAAGTCTGAAAATCCCTGAGCAATTCGACATGCGATCTGGAAG 1680
*****

mp51 1681 GGCATCCTGGACCACAGGCAGCTGCACGACTTCTCCTCACCTCCTCATCTCCTGAGGACC 1740
p51B 1681 GGCATCCTGGACCACCGGCAGCTCCACGAATTCTCCTCCCCTTCTCATCTCCTGCGGACC 1740
*****

mp51 1741 CCAAGTGGTGCCTCTACCGTCAGTGTGGGCTCCAGTGAGACCCGTTGGTGAACGTGTGATC 1800
p51B 1741 CCAAGCAGTGCCTCTACAGTCAGTGTGGGCTCCAGTGAGACCCGGGGTGAGCGTGTATT 1800
*****

mp51 1801 GATGCCGTGCGCTTTACCCCTCCGCCAGACCATCTCTTTTCCACCCCGTGACGAGTGGAAT 1860
p51B 1801 GATGCTGTGCGATTACCCCTCCGCCAGACCATCTCTTTTCCACCCCGAGATGAGTGGAAT 1860
*****

mp51 1861 GATTTCAACTTTGACATGGATTCTCGTCGCAACAAGCAGCAGCGTATCAAAGAGGAAGGA 1920
p51B 1861 GACTTCAACTTTGACATGGATGCTCGCCGCAATAGCAACAGCGCATCAAAGAGGAGGGG 1920
**

mp51 1921 GAA 1923
p51B 1921 GAG 1923
**
  
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FIG. 15

mp51BnAA	M8QSTQTSEFLSPEVVFQHIWDFLEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQ	60
p51B aa	MSQSTQTNEFLSPEVVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ	60

mp51BnAA	DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120
p51B aa	DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120

mp51BnAA	SPSPAIPSN TDYPGPHSF DVSFQQSS TAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180
p51B aa	SPSPAIPSN TDYPGPHSF DVSFQQSS TAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180

mp51BnAA	PQGAVIRAMPVYKKAESHVTEVVKRCPNBELSREFNEGQIAPPSELIRVEGNSHAQYVEDP	240
p51B aa	PQGAVIRAMPVYKKAESHVTEVVKRCPNBELSREFNEGQIAPPSELIRVEGNSHAQYVEDP	240

mp51BnAA	ITGRQSVLVPIEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC	300
p51B aa	ITGRQSVLVPIEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC	300

mp51BnAA	FEARICACPGDRKADEDSIRKQQVSDSAKNGDGTKRPFQNTTEGIQMTSIRKRRSPDDE	360
p51B aa	FEARICACPGDRKADEDSIRKQQVSDSTKNGDGTKRPFQNTTEGIQMTSIRKRRSPDDE	360

mp51BnAA	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIRQQQQQQHQHLLQKQTSIQSPSSY	420
p51B aa	LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETIRQQQQQQHQHLLQKQTSIQSPSSY	420

mp51BnAA	GNSSPPLNKMNSMNKLPSVSQILNPQORNALTPPTMPEGMGANIPMMGTHMPMAGDMNGL	480
p51B aa	GNSSPPLNKMNSMNKLPSVSQILNPQORNALTPPTIPDGMGANIPMMGTHMPMAGDMNGL	480

mp51BnAA	SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY	540
p51B aa	SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY	540

mp51BnAA	SMDDLASLKIPEQFRHAIWKGILDERQLHDFSSPPLLRTPSGASTVSVGSSETRGERVI	600
p51B aa	SMDDLASLKIPEQFRHAIWKGILDERQLHEFSSPPLLRTPSASTVSVGSSETRGERVI	600

mp51BnAA	DAVRFTLRQTISFFPRDEWNTDFNEDMDSRRNKQQRKEEGE	641
p51B aa	DAVRFTLRQTISFFPRDEWNTDFNEDMDARRNKQQRKEEGE	641

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